

This listing of claims will replace all prior versions, and listings of claims in the application.

**Listing of Claims:**

Claims 1-3 (canceled).

4. (withdrawn) A method for selecting a database containing expressed genes from primate CD34+ cells, said method comprising:

(a) selecting genes whose expression level is greater than or equal to 7-fold above background in human cells; and

(b) further selecting genes selected in (a) whose expression levels differ between humans and baboons by 3-fold or less.

5. (withdrawn) The method of claim 4, wherein gene expression is measured by the gene filter method.

6. (withdrawn) A computer system comprising:

(a) a database containing nucleotide sequences pertaining to a plurality of biomolecular sequences selected in accord with the method of claim 4;

(b) a first hierarchy of function categories into which at least some of said biomolecular sequences are grouped;

(c) a user interface allowing a user to selectively view information regarding said plurality of said biomolecular sequences as it relates to said first hierarchy.

7. (withdrawn) The computer system of claim 7, wherein the biomolecular sequences are selected from the group consisting of ESTs, full length sequences, and combinations thereof.

8. (withdrawn) The computer system of claim 7, wherein the user interface allows the user to selectively view information regarding a subset of said plurality of said biomolecular sequences which subset is grouped in both a selected category and for a selected application.

9. (withdrawn) A computer implemented method for managing information relating to hematopoietic analyses said method comprising:

(a) a first identifier identifying a target sample applied to a probe array chip;

(b) a second identifier identifying said probe array chip to which said target sample was applied; and

(c) creating an electronically stored chip table, said chip table storing a record for said polymer probe array chip, said chip record comprising

- i) a plurality of fields storing at least one of a plurality of data identifiers, including:
- ii) said second identifier identifying said probe array chip, and
- iii) a third identifier specifying a layout of probes on said probe array chip.

10. (withdrawn) A database method for analyzing hematopoietic tissue said method comprising:

(a) providing a first database comprising a first plurality of records, one for each of a plurality of cDNA sequences, said records having at least one of a plurality of fields storing:

- i) a first attribute identifying a target sample applied to a probe array chip;
- ii) a second attribute identifying said probe array chip to which said target sample

was applied; and

(a) providing a second database comprising a second plurality of records for said probe array chip, said records having at least one of a plurality of fields storing:

- (i) said second attribute identifying said probe array chip; and
- (ii) a third attribute specifying a layout of probes on said probe array chip.

11. (withdrawn) The database method for analyzing gene expression information of claim 10, wherein said first database and said second database are relational database tables.

12. (currently amended) A microchip comprising a plurality of cDNA molecules, wherein a majority of the DNA molecules are expressed in hematopoietic cells tissue of a primate, the molecules selected for an analysis of expression levels in a hematopoietic tissue.

13. (currently amended) The microchip of claim 12, wherein the hematopoietic tissue is selected from the group consisting of bone marrow, peripheral blood, stem cells, transplanted marrow, and leukemia cells from human and ~~related~~ primates including baboon.

14. (currently amended) The microchip of claim 12, wherein the plurality of cDNA molecules is designated by the term cdna id whose GenBank accession numbers are denoted by the term acc unique identifiers as shown in Appendix A.

15. (currently amended) The microchip of claim ~~13~~ 14, wherein the plurality of cDNA molecules is designated by a subset of the cdna id whose GenBank accession numbers are denoted by acc unique identifiers as shown in Appendix A.

16. (currently amended) The microchip of claim 12, wherein the expression analysis is to determine if prior to transplantation, a bone marrow transplant will engraft for transplantation by comparing expression levels of the DNA molecules in the transplant and a host.

17. (currently amended) The microchip of claim 12, wherein the expression analysis is to determined if expand a stem cell graft needs to be expanded *ex vivo*.

18. (currently amended) The microchip of claim 12, wherein the expression analysis is to determine changes in gene expression in hematopoietic cells following a pharmacological manipulations treatment.

19. (currently amended) The microchip of claim 12, wherein the expression analysis is to identify ~~novel~~ genes ~~involved in~~ relevant to hematopoiesis.

20. (currently amended) The microchip of claim 12, ~~wherein the analysis is to diagnose hematopoietic cancers.~~ 10. The microchip of claim 1, wherein the expression analysis is to determine if ~~modifications~~ gene therapy altered expression levels of the cDNA molecules in the microchip.

21. (currently amended) The microchip of claim 20 12, wherein the expression analysis is to determine if modifications include gene therapy and treatment with growth factors altered expression levels of the cDNA molecules in the microchip.

22. (currently amended) A microchip comprising a data set selected from a database, the data set comprising nucleotide sequences of a plurality of cDNA molecules expressed in hematopoietic ~~cells~~ tissue, the molecules selected for an expression analysis of hematopoietic tissue.